

Fig.1

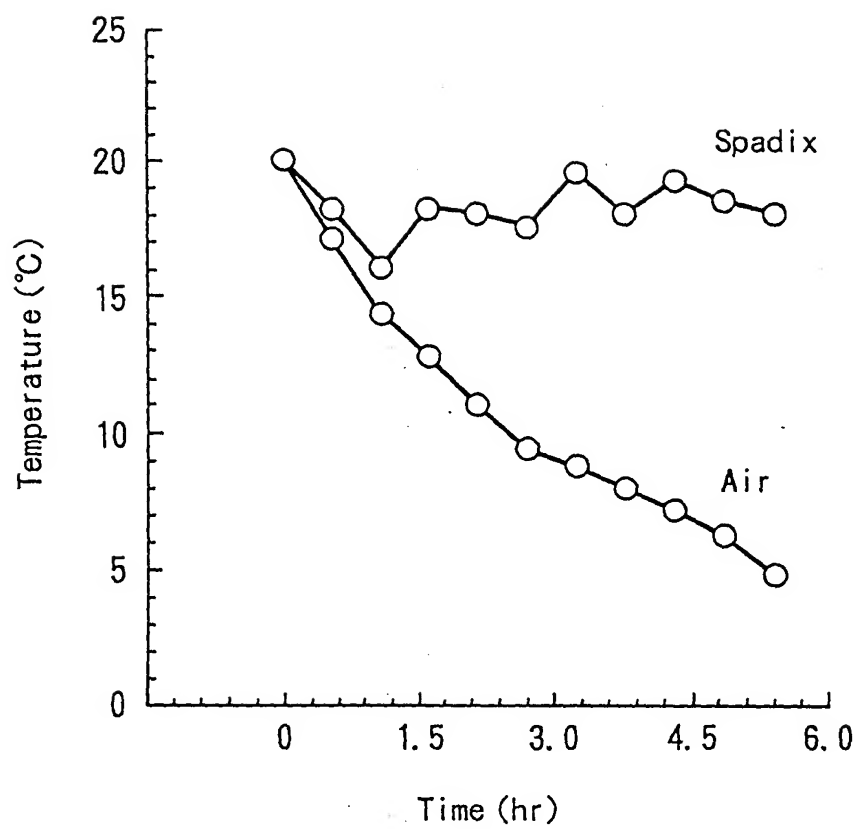


Fig.2

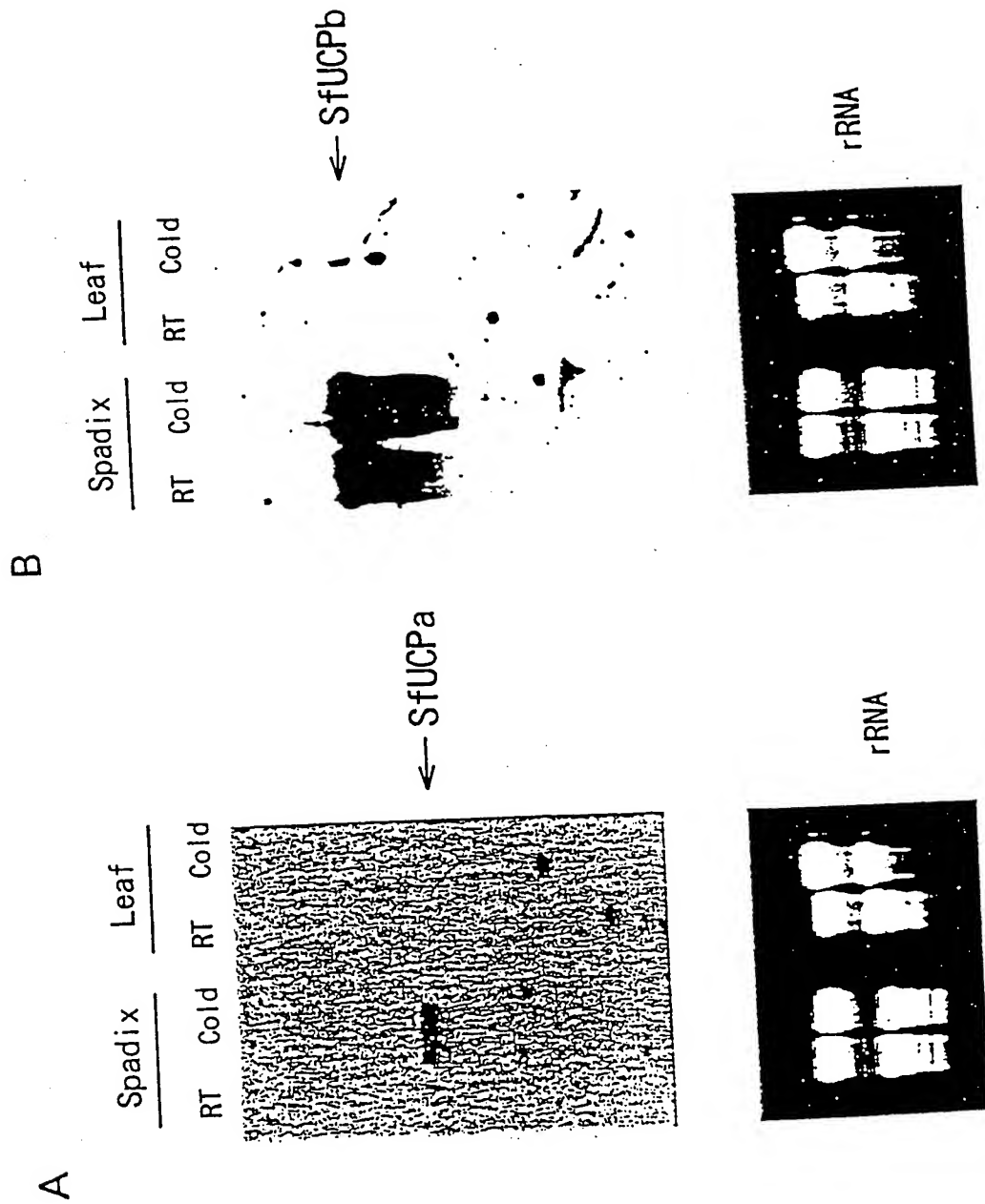


Fig.3 Top

I

SfUCPA	1	---MGDHGPRTEISFAGSSR-AAFAACFAELCT	PLDTAKVRLQLQKRAVTGDV-VALPKY	56
SfUCPB	1	---MGDHGPRTEISFAGSSR-AAFAACFAELCT	PLDTAKVRLQLQKRAVTGDV-VALPKY	56
StUCP	1	MGGDHGGKSDISFAGIFASSAFACFAEACTIP	LDTAKVRLQLQKRAVEGCG-LALPKY	59
AtPUMP	1	---MVAAGKSDLSLPKTFACSAFACVGEVCTIP	LDTAKVRLQLQKSAFTLAGDVTLPKY	57
human UCP1	1	-MGGLTASDVHPTLVGVQLFSAP IAACLADVI	THPLDTAKVRLVQQGECPP---TSSVIRY	55
human UCP2	1	-MVGFKATDVPPPTATVKFLGAGTAACIADLI	THPLDTAKVRLIQGESQCPVRATASAQY	59
human UCP3	1	-MVGLKPSDVPPTMAVKFLGAGTAACFADLV	THPLDTAKVRLIQGENQ-AVQTARLVQY	58

II

SfUCPA	57	RGMLGTVATIAREEGLSALHWKGI	VPGLHRQCLFGGLRIGLYEPVKSFYVG--DNFVGDI	P 114
SfUCPB	57	RGMLGTVATIAREEGLSALHWKGI	VPGLHRQCLFGGLRIGLYEPVKSFYVG--DNFVGDI	P 114
StUCP	60	RGLLGTVGTIAKEEGLASLHWKGI	VPGLHRQC IYGGCLRIGMYEPVKNLYVG--KDHVGD	VP 117
AtPUMP	58	RGLLGTVGTIAAREEGLRSLHWKGV	VPGLHRQCLFGGLRIGMYEPVKNLYVFTGKDFVGD	VP 117
human UCP1	56	KGVLGTITAVVKTTEGRPKLYSGLP	AGLQRQISSASLRIGLYDVTVQEFFLTA---GKETAPS	112
human UCP2	60	RGVMGTILTMVRTGPRSLYNGLV	AGLQRQMFSASVRIGLYDSVKQFYT-----KGSEHAS	115
human UCP3	59	RGVLGTILTMVRTGPRCSPYNGLV	AGLQRQMFSASIRIGLYDSVKQVYTP---KGADNSS	115

3-2/8

IV

V

IV

172	GLGALWTTGLGPNLARNAI	INAAELASYDQVKQTILKLP	GSDNIFTHILAG--	LGAGFFA	229
172	GLGALWTTGLGPNLARNAI	INAAELASYDQVKQ-----	-----	-----	203
175	GVRALWTTGLGPNIGRNAI	INAAELASYDQVKEAVLRIP	GFTDQNVVTHLIAG--	LGAGFFA	232
177	GVRALWTTVLGPNVARNAI	INAAELASYDQVKETILKIP	GFTDQNVVTHILSGLFT	GAGFFA	236
169	GLTGLWKGTTPNLMRSVI	INCTELVTYDLMKEAFVKNNI	LADDPCHLVSA--	LIAGFCA	226
171	GFRGLWKGTSPNVARNAI	VNCAELVTYDLIKDALLKANL	MTDPLCHFTSA--	FGAGFCT	228
174	GVRGLWKGTLPNIMRNAI	VNCAEVVTYDILKEKLDDYHLL	TDNFPCHFVSA--	FGAGFCA	231

Fig.3 Down

VI

SfUCPA	230	VCIGSPVDVVKSRAMGDS--AYKSTFDCFIKTLKNDGLLAFYKGFIPNFGRLG--SNNVI	285
SfUCPB	204	-----MKSRAMGDS--AYKSTFDCFIKTLKNDGPLAFYKGFIPNFGRLG--SNNVI	250
StUCP	233	VCIGSPVDVVKSRAMGDS--AYKNTLDCFVKTLKNDGPLAFYKGFIPNFGRLG--SNNVI	288
AtPUMP	237	VCIGSPVDVVKSRAMGDS--AYKGTIDCFVKTLKSDGPHAFYKGFIPNFGRLGSGFTNNVI	295
human UCP1	227	TAMSSPVDVVKTRHINSPPGQYKSVNPNCAKVF TNEGPTAFFKGLVPSFLRLG--SNNVI	284
human UCP2	229	TVIASPVDVVKTRHNSALGQYSSAGHCAL TMLQKEGPRAFYKGFMPSEFLRLG--SNNVV	286
human UCP3	232	TVVASPVDVVKTRHNSPPGQYFS2LDCMIKVAQEGPTAFYKGF TPFSEFLRLG--SNNVV	289

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PNBD

SfUCPA	286	MFLTLEQVKRFFIKEVPN-----	303
SfUCPB	251	MFLTLEQVKRFFIKEVPN-----	268
StUCP	289	MFLTLEQAKKFVKSLESP-----	306
AtPUMP	296	MFLTLEQAKKYVRELDASKRN--	316
human UCP1	285	MFVCFEQLKRELSKSRQTHDCAT	307
human UCP2	289	MFVTYEQLKRALMAACTSREAPF	309
human UCP3	290	MFVTYEQLKRALMKVQMLRES PF	312

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Fig.4

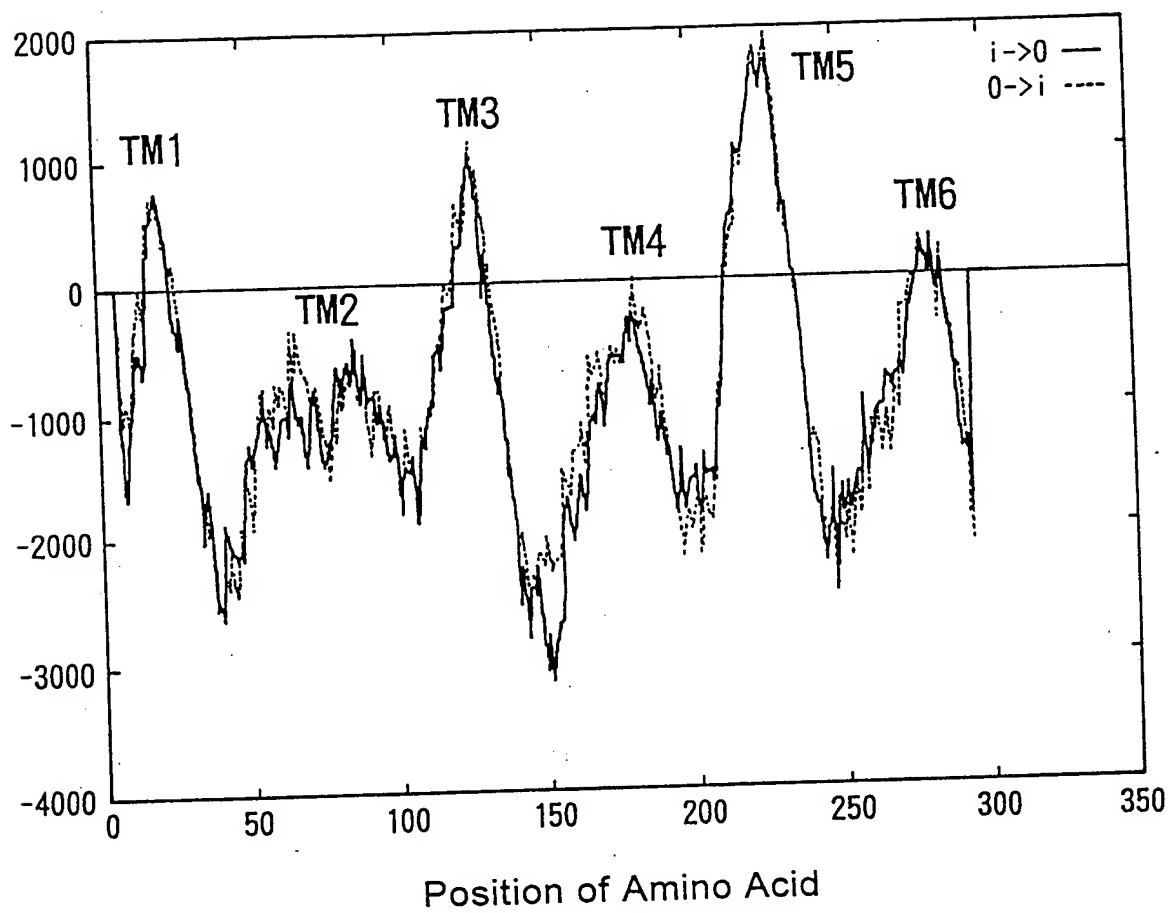


Fig.5

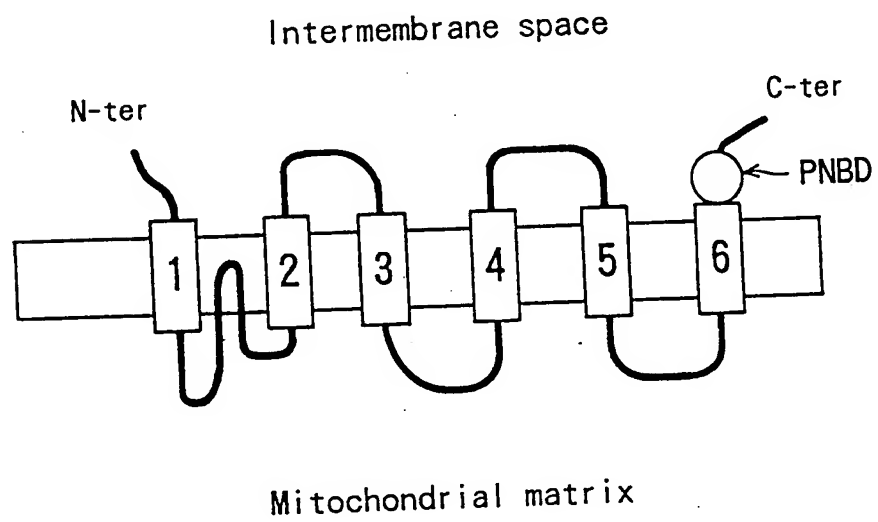


Fig.6

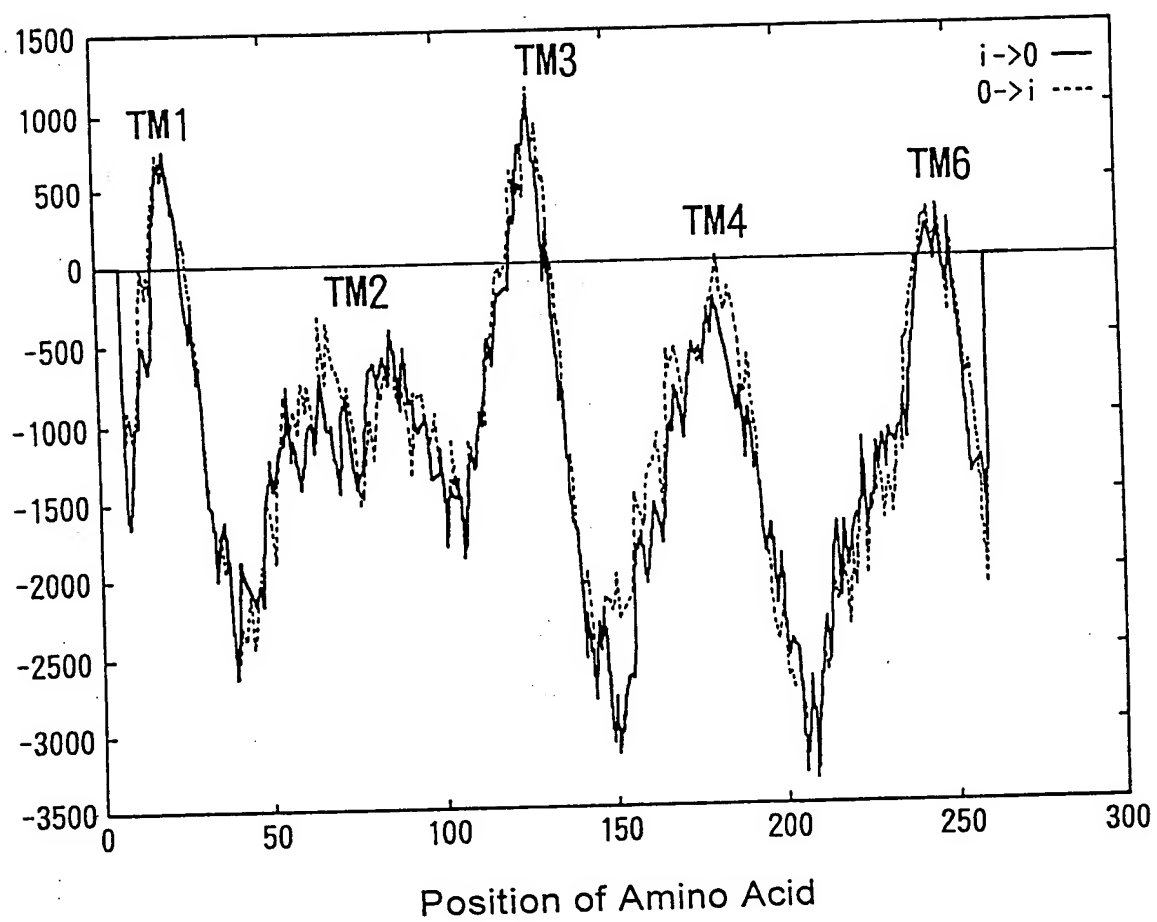


Fig.7

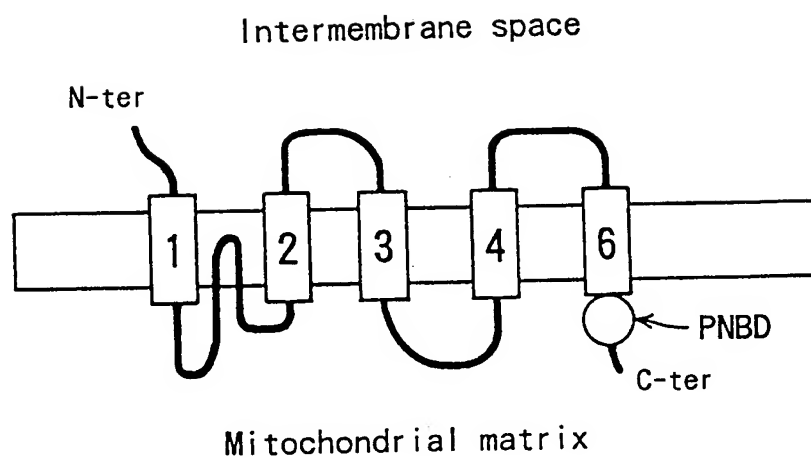


Fig.8

